1600

RAW SEQUENCE LISTING   DATE: 01/29/2003
PATENT APPLICATION: **US/09/835,147A**   TIME: 13:55:39

Input Set : **A:\2879-US RevsdSeqListing 010303.txt**
Output Set: **N:\CRF4\01292003\I835147A.raw**

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 3 <110> APPLICANT: Maliszewski, Charles R.
 4        Gayle III, Richard B.
 5        Price, Virginia L.
 6        Gimpel, Steven D.
 8 <120> TITLE OF INVENTION: INHIBITORS OF PLATELET ACTIVATION AND RECRUITMENT
10 <130> FILE REFERENCE: 2879-US
12 <140> CURRENT APPLICATION NUMBER: US 09/835,147A
13 <141> CURRENT FILING DATE: 2001-04-13
15 <150> PRIOR APPLICATION NUMBER: US 60/104,585
16 <151> PRIOR FILING DATE: 1998-10-16
18 <150> PRIOR APPLICATION NUMBER: US 60/107,466
19 <151> PRIOR FILING DATE: 1998-11-06
21 <150> PRIOR APPLICATION NUMBER: US 60/149,010
22 <151> PRIOR FILING DATE: 1998-08-13
24 <150> PRIOR APPLICATION NUMBER: PCT/US99/22955
25 <151> PRIOR FILING DATE: 1999-10-13
27 <160> NUMBER OF SEQ ID NOS: 37
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1599
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (67)..(1596)
39 <223> OTHER INFORMATION:
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P.6

ENTERED

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43 ccacaccaag cagcggctgg gggggggaaa gacgaggaaa gaggaggaaa acaaaagctg      60
45 ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc        108
46        Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
47         1           5                    10
49 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata      156
50 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
51 15                  20                  25                  30
53 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac      204
54 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
55                  35                  40                  45
57 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta      252
58 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
59                  50                  55                  60
61 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg      300
62 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
63          65                  70                  75
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65 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt    348
66 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
67     80                  85                  90
69 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa    396
70 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
71 95                  100                 105                 110
73 aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt    444
74 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
75              115                 120                 125
77 tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa    492
78 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
79              130                 135                 140
81 gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac    540
82 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
83              145                 150                 155
85 tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa    588
86 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
87     160                 165                 170
89 ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt    636
90 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
91 175                 180                 185                 190
93 cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag    684
94 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
95              195                 200                 205
97 gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act    732
98 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
99              210                 215                 220
101 ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa    780
102 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
103             225                 230                 235
105 ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg    828
106 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
107     240                 245                 250
109 tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att    876
110 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
111 255                 260                 265                 270
113 cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga    924
114 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
115             275                 280                 285
117 tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc    972
118 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
119             290                 295                 300
121 aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt    1020
122 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
123             305                 310                 315
125 att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac    1068
126 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
127     320                 325                 330
129 acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg    1116
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RAW SEQUENCE LISTING   DATE: 01/29/2003
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Input Set : **A:\2879-US RevsdSeqListing 010303.txt**
Output Set: **N:\CRF4\01292003\I835147A.raw**

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130 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
131 335             340             345             350
133 cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg    1164
134 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
135             355             360             365
137 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg    1212
138 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
139             370             375             380
141 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa    1260
142 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
143         385             390             395
145 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt    1308
146 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
147         400             405             410
149 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca    1356
150 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
151 415             420             425             430
153 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc    1404
154 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
155             435             440             445
157 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc    1452
158 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
159             450             455             460
161 cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc    1500
162 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
163         465             470             475
165 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata    1548
166 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
167     480             485             490
169 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta    1596
170 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
171 495             500             505             510
173 tag                                                                1599
176 <210> SEQ ID NO: 2
177 <211> LENGTH: 510
178 <212> TYPE: PRT
179 <213> ORGANISM: Homo sapiens
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184 1             5             10             15
187 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
188             20             25             30
191 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
192         35             40             45
195 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
196     50             55             60
199 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
200 65             70             75             80
203 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
```

```
204                  85               90               95
207 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
208                  100              105              110
211 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
212          115              120              125
215 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
216          130              135              140
219 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
220 145              150              155              160
223 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
224              165              170              175
227 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
228              180              185              190
231 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
232          195              200              205
235 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
236      210              215              220
239 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
240 225              230              235              240
243 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
244              245              250              255
247 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
248          260              265              270
251 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
252          275              280              285
255 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
256      290              295              300
259 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
260 305              310              315              320
263 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
264              325              330              335
267 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
268          340              345              350
271 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
272          355              360              365
275 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
276      370              375              380
279 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
280 385              390              395              400
283 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
284              405              410              415
287 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
288          420              425              430
291 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
292          435              440              445
295 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
296      450              455              460
299 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
300 465              470              475              480
```

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303 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
304             485                 490                 495
307 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
308             500                 505                 510
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 476
313 <212> TYPE: PRT
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Fusion construct of human CD39
319 <400> SEQUENCE: 3
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322 1               5                   10                  15
325 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
326             20                  25                  30
329 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
330             35                  40                  45
333 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
334     50                  55                  60
337 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
338 65                  70                  75                  80
341 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
342             85                  90                  95
345 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
346             100                 105                 110
349 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
350             115                 120                 125
353 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
354     130                 135                 140
357 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
358 145                 150                 155                 160
361 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
362             165                 170                 175
365 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
366             180                 185                 190
369 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
370             195                 200                 205
373 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
374     210                 215                 220
377 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
378 225                 230                 235                 240
381 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
382             245                 250                 255
385 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
386             260                 265                 270
389 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
390             275                 280                 285
393 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
394     290                 295                 300
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/29/2003
PATENT APPLICATION: **US/09/835,147A**   TIME: 13:55:40

Input Set : **A:\2879-US RevsdSeqListing 010303.txt**
Output Set: **N:\CRF4\01292003\I835147A.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 39